

Figure 1A

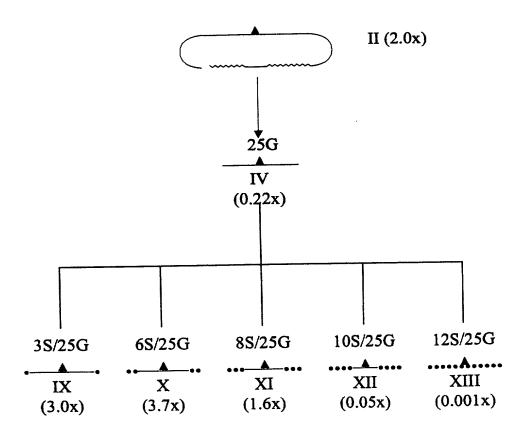


Figure 1B

EI124983108US

Plasmids, DNA targets and chimeric oligonucleotides

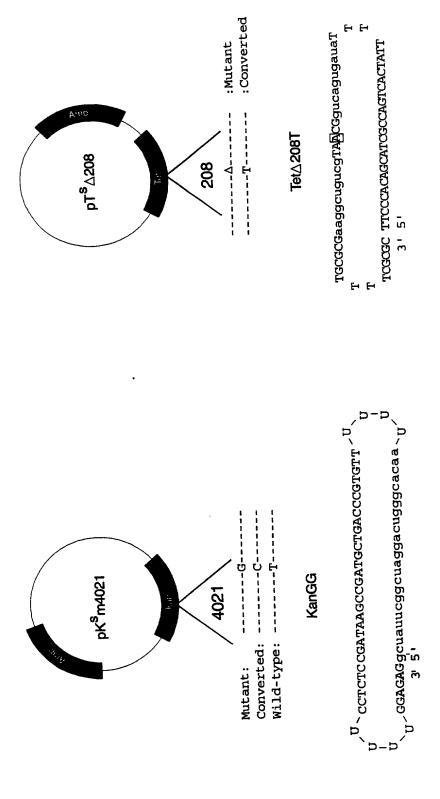


Figure 1C

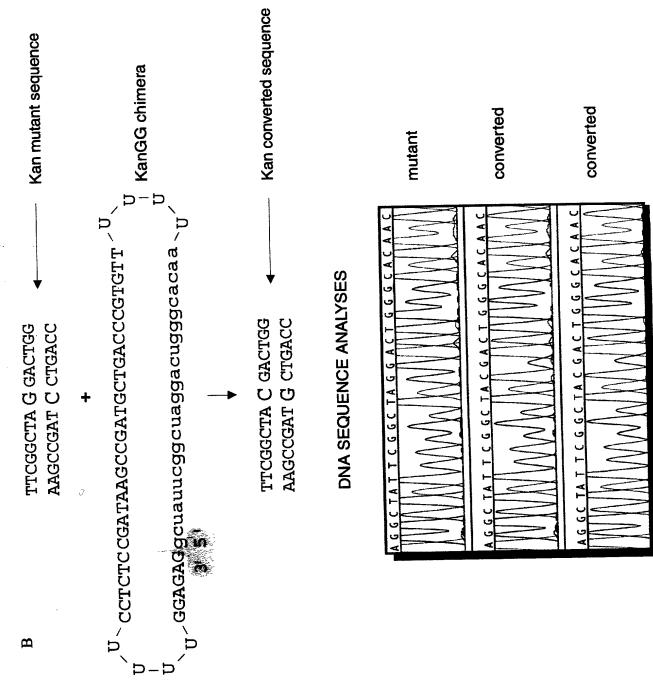


Figure 1D

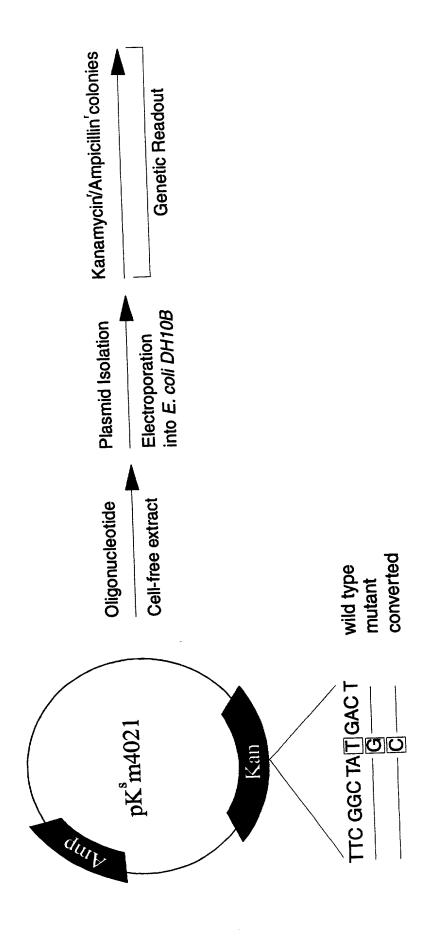
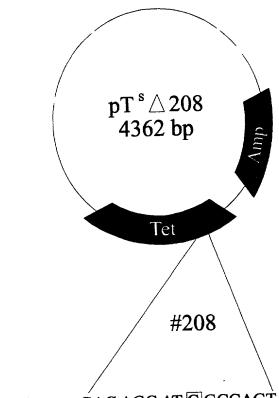


Figure 2



Wild type: GAC AGC AT CGCCAGT
Mutant: GAC AGC AT GCCAGT
Converted: GAC AGC AT TGCCAGT

Sequence analysis of Tet^r plasmid △208

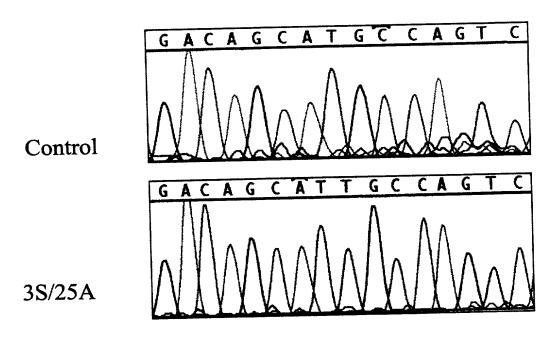


Figure 3

DNA sequence analysis of Kan^r plasmids

Target codon distri	ibution			_	
oligomer	TAG	TAC	TAC/TAG	TGG	TCG
1) 3S/25G (20)		+	95 m 46 W		
2) 6S/25G (20)		+			
3) 8S/25G (20)		+	egg mitolik did	****	
4) 10S/25G (18)		+	-	+(2)	+(2)
5) 25S/25G (4)			+(2)	+(2)	

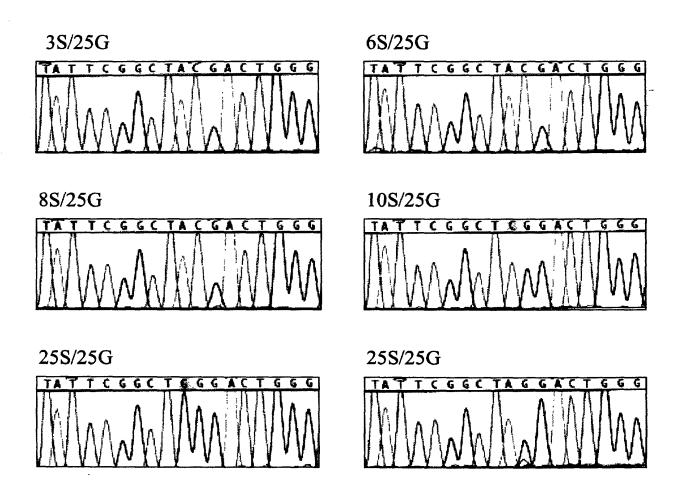


Figure 4

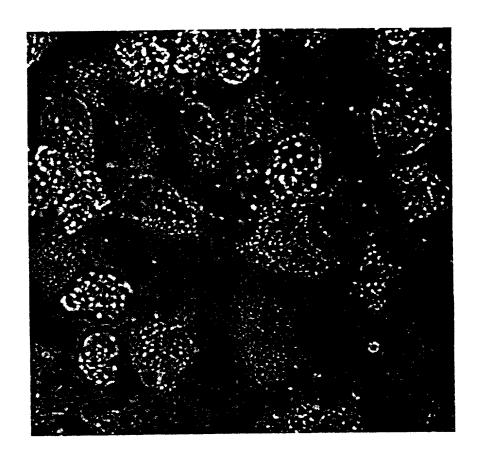


Figure 5

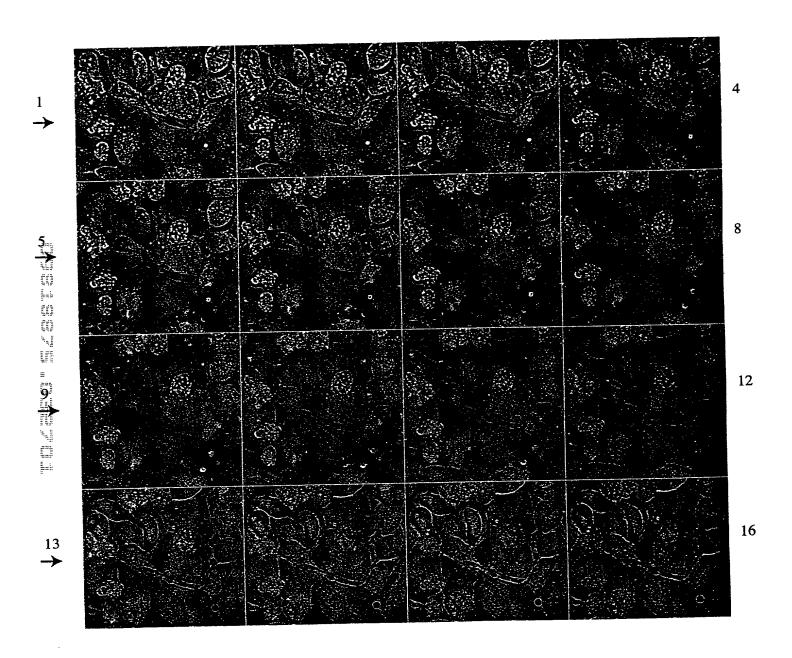


Figure 6

GIGGATAATGICCI Sequence of normal allele: GTGGATATGTCCT Target/existing mutant: Desired alteration:

GTGGATACGTCCT

Figure 7A

pAURHYG(x)EGFP

Sequence of normal allele: GTGGATATGTCCT GTGGATAGGTCCT GTGGATACGTCCT Target/existing mutant: Desired alteration:

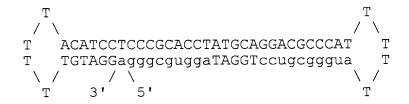
mutation at position 137 of the hyg coding region

Figure 7B

HygE3T/25: 5'-AGG GCG TGG ATA CGT CCT GCG GGT A-3'

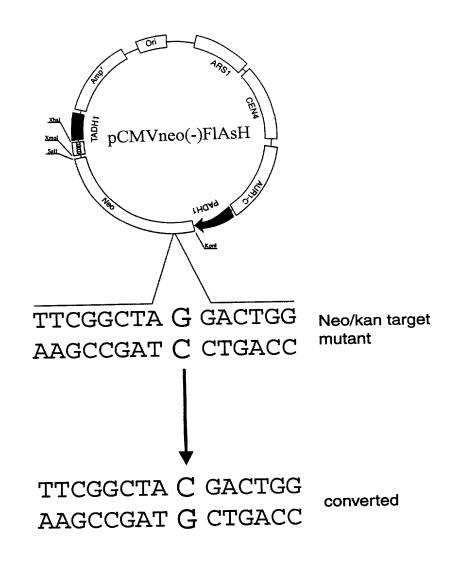
 $\frac{\text{HygE3T}/74:}{\text{GTG GTG CTT TCA GCT TCG ATG TAG GAG GGC}}$ $\frac{\text{S'-CTC}}{\text{GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG}}{\text{CCG ATG GTT TCT}}$ $\frac{\text{AC-3'}}{\text{AC-3'}}$

HygGG/Rev:



Kan70T: 5'-CAT CAG AGC AGC CAA TTG TCT GTT GTG CCC AGT CGT AGC CGA ATA GCC TCT CCA CCC AAG CGG CCG GAG A-3'

Figure 8



FUSION GENE FOR LIGAND BINDING

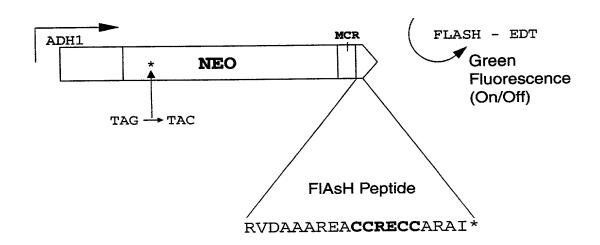


Figure 9

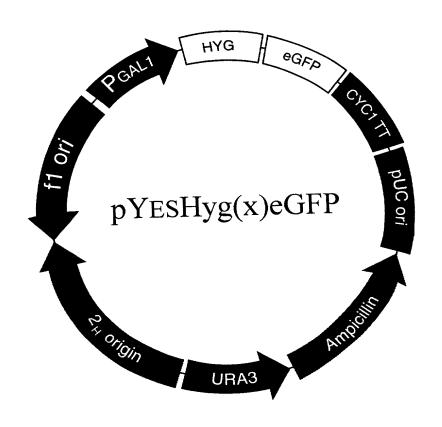


Figure 10